

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 3, 2005, 13:53:07 ; Search time 117.153 Seconds  
(without alignments)  
2342.472 Million cell updates/sec

Title: US-09-989-339A-2  
Perfect score: 3905  
Sequence: 1 MASHIVGYPRMGPRKRLKFA.....ALTNVTSATKLIQTQLASAK 765

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_23Sep04: \*  
1: geneseqp1980s: \*  
2: geneseqp1990s: \*  
3: geneseqp2000s: \*  
4: geneseqp2001s: \*  
5: geneseqp2002s: \*  
6: geneseqp2003as: \*  
7: geneseqp2003bs: \*  
8: geneseqp2004s: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	3905	100.0	765	6	ADB23036	Adb23036 Corn meth
2	3697.5	94.7	766	6	ADA48608	Ada48608 Rice prot
3	3535	90.5	765	6	ADB23040	Adb23040 Tobacco m
4	3502	89.7	765	6	ADB23045	Adb23045 Madagasca
5	3472	88.9	765	5	ABB93994	Abb93994 Herbicida
6	3472	88.9	765	5	ABB93525	Abb93525 Herbicida
7	3467	88.8	765	7	ADE25084	Ade25084 Plant gro
8	3448	88.3	765	3	AAG53127	Aag53127 Arabidops
9	3448	88.3	765	3	AAG18607	Aag18607 Arabidops
10	3448	88.3	765	5	ABB92196	Abb92196 Herbicida
11	3395	86.9	763	6	ADB23038	Adb23038 Soybean m
12	3394	86.9	755	3	AAG18608	Aag18608 Arabidops
13	3394	86.9	755	3	AAG53128	Aag53128 Arabidops
14	3357.5	86.0	728	6	ADA48634	Ada48634 Rice prot
15	3269.5	83.7	768	6	ADA48100	Ada48100 Rice prot
16	3215	82.3	717	3	AAG18609	Aag18609 Arabidops
17	3215	82.3	717	3	AAG53129	Aag53129 Arabidops
18	3194.5	81.8	684	6	ADA48126	Ada48126 Rice prot
19	3185	81.6	745	3	AAG27788	Aag27788 Arabidops
20	3131	80.2	735	3	AAG27789	Aag27789 Arabidops
21	3108.5	79.6	807	5	ABB93567	Abb93567 Herbicida
22	2952	75.6	697	3	AAG27790	Aag27790 Arabidops
23	2076	53.2	451	7	ABM73900	Abm73900 DNA clone
24	2060	52.8	446	7	ABM74475	Abm74475 DNA clone
25	2057.5	52.7	474	3	AAG39450	Aag39450 Arabidops

26	2003.5	51.3	464	3	AAG39451	Aag39451 Arabidops
27	1833	46.9	758	5	AAU72946	Aau72946 Neisseria
28	1833	46.9	758	5	AAU72999	Aau72999 Neisseria
29	1833	46.9	758	5	AAU72972	Aau72972 Neisseria
30	1824	46.7	758	3	ADP08261	Adp08261 Neisseria
31	1820.5	46.6	426	3	AAG39452	Aag39452 Arabidops
32	1818	46.6	771	6	ABP79516	Abp79516 N. gonorr
33	1776	45.5	768	7	ADF05473	Adf05473 Bacterial
34	1773.5	45.4	794	7	ABO83078	Abob83078 Pseudomon
35	1763	45.1	759	6	ABM68367	Abm68367 Photorhab
36	1757.5	45.0	767	8	ADP99011	Adp99011 C. albica
37	1756.5	45.0	760	7	ABO61538	Abob61538 Klebsiell
38	1714	43.9	765	5	ABB48512	Abb48512 Listeria
39	1694.5	43.4	767	7	ADK63384	Adk63384 Disease t
40	1686	43.2	767	5	ABP65725	Abp65725 Bifidobac
41	1674.5	42.9	759	5	ABB54591	Abb54591 Lactococc
42	1673	42.8	749	8	ADK46406	Adk46406 Streptoco
43	1663	42.6	745	4	AAG91007	Aag91007 C glutami
44	1663	42.6	745	5	AAM51073	Aam51073 Corynebac
45	1660	42.5	749	6	ABU00960	Abu00960 S. pneumo

ALIGNMENTS

RESULT 1	
ADB23036	
ID ADB23036	standard; proteain, 765 AA.
XX	
AC ADB23036;	
XX	
DT 20-NOV-2003	(first entry)
XX	
DE	Corn methionine synthase.
XX	
KW	enzyme; plant; methionine synthase; methionine; seed; transformed plant;
KW	transgenic; corn.
XX	
OS	Zea mays.
XX	
PN	US2003088886-A1.
XX	
PD	08-MAY-2003.
XX	
PF	28-JAN-2002; 2002US-009893339.
XX	
PR	30-AUG-1995; 95US-0002973P.
PR	27-AUG-1996; 96US-00703829.
PR	19-AUG-1999; 99US-00377431.
XX	
PA	(FALC/) FALCO S C.
PA	(FAMO/) FAMODU O O.
PA	(RAFA/) RAFALSKI J A.
PA	(RAMA/) RAMAKER M L.
PA	(TARC/) TARCZYNSKI M C.
PA	(THOR/) THORPE C.
XX	
PI	Falco SC, Famodu OO, Rafalski JA, Ramaker ML, Tarczynski MC;
PI	Thorpe C;
XX	
DR	WPI; 2003-657990/62.
DR	N-PSDB; ADB23035.
XX	
PT	New nucleic acid fragments encoding a plant 5-methyltetra-
PT	hydropteroyltriglutamate-homocysteine methyl transferase or methionine
PT	synthase, useful for producing increased levels of methionine in the
PT	seeds of transformed plants.
XX	
PS	Example 1; Fig 2; 69pp; English.
XX	
CC	The invention relates to an isolated nucleic acid fragment encoding a
CC	plant methionine synthase. The nucleic acid fragments and chimeric genes
CC	are useful for producing increased levels of methionine in the seeds of

CC transformed plants. The present sequence represents the amino acid  
CC sequence of a plant methionine synthase.

**SQ Sequence 765 AA;**

Query Match	100.0%;	Score 3905;	DB 6;	Length 765;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 765;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

```
Qy      1 MASHIVGYPRMGPKRELKFALESFWDGKSSAEDLEKVATDLRSSIWKOMSEAGIKYIPSN 60
        |||||
Db      1 MASHIVGYPRMGPKRELKFALESFWDGKSSAEDIEKVATDLRSSIWKOMSEAGIKYIPSN 60
```

Qy	61 TSSYYDQVLDTAMLGAVPERYSWTGEGIGLSTYFSMARGNATVPAMEMTKMPDNVHFI 120 
Db	61 TSSYYDQVLDTAMLGAVPERYSWTGEGIGLSTYFSMARGNATVPAMEMTKMPDNVHFI 120 

[illegible]

QY 181 IGSILPIYKEVVAELKAGASWIOLEPTLVKDLDAHELAFSSAYAELESSFSGINVTI 240  
|||||  
Db 181 IGSILPIYKEVVAELKAGASWIOLEPTLVKDLDAHELAFSSAYAELESSFSGINVTI 240  
|||||

QY 241 ETVFADIPAESYKLTLSGVATAYGFDLIRGAKTLDLIRSSFPSGKYLFAGVVDENIWA 300  
|||||  
DB 241 ETVFADIPAESYKLTLSGVATAYGFDLIRGAKTLDLIRSSFPSGKYLFAGVVDENIWA 300  
|||||

QY	301	DDLAASLTLSLEAVAGKDKLVSTSCSLMHTAVDLVNETKLDDEIKSWLAFAAKVYE	360
Db	301	DDLAASLTSTHSLEAVAGKDKLVSTSCSLMHTAVDLVNETKLDDEIKSWLAFAAKVYE	360

	QY	361 VNALAKLAGÖKDEVYFAAANAQAASPRSSPVRTNEEVÖKAHAALRGSDHRRSTTVSARL 420
Dh	361 VNALAKALAGOKDEVYFAAANAQAASPRSSDPVRTNEEVOKAHAALRGSDHRSPSTTVSABT. 420	

421 DAQOKLNLVLPPTTIGSFPOTVELRVRREYKAKKITEDEYISAIKEISKVKIQEE 480

[illegible]

QY 541 FWSKMAQSMTPRPMKMLTGPVITILNWSFVRNDQPRFETCYQIALAIKKEVEDLEAGIQ 6000

QY 601 VIQIDEALLREGPLRKSEHAFYLDMAVHSFRITNGVQDQTQIHTHMCYSNFDLIHSI 660

QY 661 IDMDADVITIENSRDEKLLSVFREGVYGAGIGPGVYDIHSPRI PSTEEIADRYEKMLA 720

QY 721 VFDNIIWNPDCGLKTRKYTEVKPALTNMVSATKLI RTOLASAK 765  
|||||

RESULT 2  
ADA48608  
ID ADA48608 standard; protein; 766 AA.

AC	ADA48608;
XX	
DT	20-NOV-2003 (first entry)

DE Rice protein conferring disease resistance in plants.

KW disease resistance; pathogen tolerance; plant pathogen; plant; rice.

XX  
OS      *Oryza sativa.*

PN WO2003000906-A2.

PD	03-JAN-2003.
XX	
PF	21-JUN-2002; 2002WO-1B002453.

PR 22-JUN-2001; 2001US-0300112P.  
PR 26-SEP-2001; 2001US-0352277P.  
PR 22-MAR-2002; 2002US-0366535P.

PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
XX  
PI Glazebrook J, Briggs S, Cooper B, Goff SA, Moughamer T;

XX	WPI; 2003-184052/18.
DR	
DR	N-PSDB; ADA48607.

PT New polynucleotide comprising a plant nucleotide sequence having an open  
PT reading frame that encodes a polypeptide associated with disease  
PT resistance, useful for conferring resistance or tolerance to a plant

F1 pathogen:  
XX  
PS claim 10: SEO ID NO 678: 299pp: English.

255 The invention relates to a novel isolated polynucleotide comprising a  
256 plant nucleotide sequence having an open reading frame that encodes a  
257 polypeptide associated with disease resistance or its fragment having

CC conferring disease resistance used in the invention.

**SQ Sequence 766 AA;**

Query Match	94.7%;	Score 3697.5;	DB 6;	Length 766;
Best Local Similarity	93.5%;	Pred. No. 4.4e-301;		
Matches 716;	Conservative 28;	Mismatches 21;	Indels 1;	Gaps 1;

```
Oy      1 MASHIVGYPRMGPKRELKFALESFWDGKSSADELEKYATDLRSSIWKMOMSEAGIKYIPSN 60
|||||
Db      1 MASHIVGYPRMGPKRELKFALESFWDGKSADDELEKYATDLRASIMWQMADAGIKYIPSN 60
```

Qy 61 TSSYYDQVLDTTAMLGAVPERYSWTGCEIGLSTYFSMARGNATVPAMEWTKMEDNTNYHFI 120  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 61 TFSYYDOVLDTAAMLGAVERYSWTGCEIGFSTYFSMARGNATVPAMEWKMFEDNTNYHFI 120

QY	121	VPELGPTKFTYASHKAVSEYKEAKALGIDTVPLVGPVSYLLLSKPAKGVKSFSLISL	180
		:     :     :     :     :     :     :     :     :	
Db	121	VPELGPTKFSYSSHKAVNEYEKAKALGDTVPLVGPVSYLLLSKPAKGVKSFALLISL	180

QY 181 LGSILPIYKEVVAELKAAGASWIODEPTLVKDLDAHELAAFSAYAELESFSGINVL 2400  
| | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | :  
Db 181 ISSIIPYKKEVIATLKAAGATWIOFEPTLVLDLSHOLAFASSAATTELESAISGINVL 2400

QY 241 ETYFADIPAESYKLTLSGVTAYGFDLIRGAKTLDLIRSS-FPSGKYLFAGVVDGRNIW 299  
|||||:|||||:|||||  
Db 241 ETYFADIPAESYKLTLSNSYTPYVGFDLIRGAKTLDLIRSGAFPSGKYLFAGVVDGRNIW 300  
|||||:|||||:|||||

```

QY      300  ADDLAASLTLSLEAVAGKDKLVSTSCSLMHTAVDLVNETKLDDEIKSNLAPAAQKV  359
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB      301  ADDLAASLTLSLEAVAGKDKLVSTSCSLMHTAVDLVNETKLDDEIKSNLAPAAQKV  360
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

```

QY 360 EYNALAKALAGOKDEVFYFAANAAAQASRRSSPRVTNEEVOKAAALRGSDHRRSTTVSAR 4199  
 361 EYNALAKALAGOKDEVFYFAANAAAQASRRSSPRVTNEEVOKAAALRGSDHRRSTTVSAR 4200

QY 420 LDAQQKLNLPVPTTIGSFQTVELRVRREYKAKKITEDEYISAIKEEISKVKIQE 479

Db 421 LDAQQKLNLPVLPYTTIGSFPTVELRRVREYKAKKISEEYISAIKEISKVKIQE 480

OY	480	EELDIDLVLHGEPPERNDMVEYFGEQLSGFAFTANGWVQSYGSRCKPPIIYGDVSRPNBMT	5339
Dd	481	EELDIDLVLHGEPPERNDMVEYFGEQLSGFAFTANGWVQSYGSRCKPPIIYGDVSRPNBMT	5400
OY	540	VFWSKMAQSMTPRPMKMLTGPTVITLWNSFVRNDQPRFETCYOIALAIKKEVEDLEAGI	5999
Dd	541	VFWSKLAQSMTSRPMKGMLTGPVTILWNSFVRNDQPRFETCYOIALAIKKEVEDLEAGI	6000
OY	600	QVIQIDEAALREGPLRKSEHAFLDMAVHSFRITNCGVODTTQIHTHMCYSNFENDIIHS	6599
Dd	601	QVIQIDEAALREGQLRKAHAHFYLDMAVHSFRITNCGVODTTQIHTHMCYSNFENDIIHS	6600
OY	660	IIDMDADVITIENSRSDEKLISVFREGVKYGACIGPGVYDIHSPRIIPSTEEIADRVKML	7199
Dd	661	IIMDDADVITIENSRSDEKLISVFREGVKYGACIGPGVYDIHSPRIIPSTEEIADRVNKM	7200
OY	720	AVFDTNILMVNPDCGLKTRKYTEVKPALTNVSAATKLIRTOLASAK 765	
Dd	721	AVLDTNILMVNPDCGLKTRKRYNEVKPALTNVSAKLIIRTOLASAK 766	

RESULT 3  
ADB23040  
ID ADB23040 standard; protein; 765 AA.

AC	ADB23040;
XX	
DT	20-NOV-2003 (first entry)

DE Tobacco methionine synthase.

KW enzyme; plant; methionine synthase; methionine; seed; transformed plant;  
KW transgenic; tobacco.

**OS**    **Nicotiana tabacum.**

PN US2003088886-A1.

PD 08-MAY-2003.

PF 28-JAN-2002; 2002US-00989339.

PR 30-AUG-1995; 95US-0002973P.

PR 19-AUG-1999; 99US-00377431.

PA (FALC/) FALCO S. C.

PA (RAFA/) RAFALSKI J A.

PA (TARC/) TARCZYNSKI M C.

XX 1999

PI Thorpe C;

DR WPI; 2003-657990/62.

XX

PT hydropteroyltriglutamate-homocysteine methyl transferase

PT seeds of transformed plants.

PS Example 1; Fig 2; 69pp; English.

CC The invention relates to an isolated nucleic acid fragment encoding a

CC are useful for producing increased levels of methionine in the seeds of

CC' sequence of a plant methionine synthase.

**SQ Sequence 765 AA;**

Query Match	90.5%	Score 3535;	DB 6;	Length 765;
Best Local Similarity	88.5%	Pred. No. 2e-287;		
Matches 677;	Conservative 38;	Mismatches 50;	Indels 0;	Gaps 0;

[illegible]

```

Qy      61 TSSYYDQVLDTTAMLGAVPERYSWTGGEIGLSTYFSMARGNATVPAMEMTKMFDTNYHFI 120
        |||||:|||||
Db      61 TFSYYDQVLDTTAMLGAVPARYNMAGEIAFDTYFSMARGNASVPAMEMTKMFDTNYHFI 120

```

```
QY      121 VPELGPSTKFTYASHKAVSEYKEAKALIGDTPVLVGPVSYLLLSKPAKGVESFSLSL 1800
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB      121 VPELGPDVNFYSYASHKAVDEYKEAKGLGVDTPVLVIGPVSYLLLSKPAKGVESFPLSL 1800
```

```
OY      181 LGSILPIYKEVVAELKAGASWIODEPTLVKDLDAHELAAFPSSAYAELESSTSGINVLI 2400
          :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      181 LDKVLPIYKEVIAELKAGASWIOFDEPTLVLDLQAHLAFTKAYAELESSTSGINVLT 2400
```

```

Qy      241 ETYPADIPAESYKLTLSGVTAVGFDLIRGAKTLDLIRSSFPSGKYLEFAGVVDGNIWA 3000
        |||||::|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      241 ETYPADVPAEAFKLTLTALKGVTAFGEFLVRGAQTLDLIRGGFPSGKYLEFAGVVDGNIWA 3000

```

```
QY      301 DDLAASLTLSLEAVAGCKDLVSTSCSLMHTAVDLVNETHKLDDEIKSWLAFPAQKVE 360
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      301 NDLAASLNLQSLGIVGKDKLVSTSCSLHTAVDLVNETHKLDDEIKSWLAFPAQKVE 360
```

[illegible]

```

QY      421 DAQOKKLNLPVLTPTTIGSFPGYVELRVRVREYKAKKITEDEYISAIKEEISKVKIQEE 4800
      |||||
      421 DAQOKKLNLPVLTPTTIGSFPGYVELRVRVREYKAKKISEEYVKAIKAEIKKVDLQEE 4800
      |||||
Db

```

<b>QY</b>	481 LDIDVLVHGEPERNDMVEYFEGEQLSGFAFTANGWVS YGSRCKPPIIYGDSRPNPMTV 5400
<b>Db</b>	481 LDIDVLVHGEPERNDMVEYFEGEQLSGFAFTANGWVS YGSRCKPPIIYGDSRPNPMTV 5400

```
QY      541 FWSKMAQSMTPRPMKGMLTGPVTLLNWSFVRNDQPREFETCYOTALAIKEVEDELEAGIQ   6000  
        ||| |  
Db     541 FWSKTAAQSMTKRPMKGMLTGPTVILLNWSFVRNDQPRFETCYOTALAIKDEVEDLEKAGIT   6000
```

```

QY      601 VIQIDEALREGPLRKSEHAFLDWAHVSFRITNCGVDTQIHTHMCYSNNDIIHSI 660
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      601 VIQIDEALREGPLRKAHAFLNMAVHVSFRITNVIQDTQIHTHMCYSNNDIIHSI 660

```

QY	661	IDMDADVITIENSRSDEKLVSFREGVKYGGAGIGPGVYDIHSPRIPSTEEIADRVEKMLA	7200
Db	661	IDMDADVITIENSRSDEKLVSFREGVKYGGAGIGPGVYDIHSPRIPSTEEIADRNVKMLA	7200

Oy	721 VFDNIIWNPDCGLKTRKYEVKPALTNNVSATKLIRTOLASAK	765
	:	
Db	721 VLDTNIILWNPPDCLGKTRKYAEVKPALENNVSAAKAIRTOIASSK	765

RESULT 4  
ADB23045  
ID ADB23045 standard; protein; 765 AA

AC	ADB23045;
XX	
DT	20-NOV-2003 (first entry)

DE Madagascari periwinkle methionine synthase.  
XX  
KW enzyme; plant; methionine synthase; methionine; seed; transformed plant;

OS Catharanthus roseus.

XX US2003088886-A1.  
PN  
XX 08-MAY-2003.  
PD  
XX 28-JAN-2002; 2002US-00989339.  
PF  
XX 30-AUG-1995; 95US-0002973P.  
PR 27-AUG-1996; 96US-00703829.  
PR 19-AUG-1999; 99US-00377431.  
XX  
PA (FALC/) FALCO S C.  
PA (FAMO/) FAMODU O O.  
PA (RAFA/) RAFALSKI J A.  
PA (RAMA/) RAMAKER M L.  
PA (TARC/) TARCZYNSKI M C.  
PA (THOR/) THORPE C.  
XX  
PI Falco SC, Famodu OO, Rafalski JA, Ramaker ML, Tarczynski MC;  
PI Thorpe C;  
XX  
DR WPI; 2003-657990/62.  
XX  
PT New nucleic acid fragments encoding a plant 5-methyltetra-  
PT hydropteroyltriglutamate-homocysteine methyl transferase or methionine  
PT synthase, useful for producing increased levels of methionine in the  
PT seeds of transformed plants.  
XX  
XX Example 1; Fig 2; 69pp; English.  
PS  
CC The invention relates to an isolated nucleic acid fragment encoding a  
CC plant methionine synthase. The nucleic acid fragments and chimeric genes  
CC are useful for producing increased levels of methionine in the seeds of  
CC transformed plants. The present sequence represents the amino acid  
CC sequence of a plant methionine synthase.  
XX  
SQ Sequence 765 AA;

Query Match 89.7%; Score 3502; DB 6; Length 765;  
Best Local Similarity 87.5%; Pred. No. 1.2e-284;  
Matches 669; Conservative 47; Mismatches 49; Indels 0; Gaps 0;

QY 1 MASHIVGYPRMGPKRELKFALSFMDGKSSAEDLEKVAATDRLSSIWKMSEAGIKYIPSN 60  
DB 1 MASHIVGYPRMGPKRELKFALSFMDGKSSAEDLQKVAADLRSSIWQMADAGIKYIPSN 60  
QY 61 TSSYYDOVLDTTAMLGAVPERYSWTGGEIGLSTYFSMARGNATVPAMEMTKMFDTNVHFI 120  
DB 61 TFSYYDOVLDTATMLGAVPPRYNFAGGEIGFDTYFSMARGNASVPAMEMTKMFDTNVHYI 120  
QY 121 VPGLGSTKFTYASHKAVSEYKEAKALGIDTVPVLVGPVSYLLSKPAKGVESFSLSL 180  
DB 121 VPGLGEVNFYSYASHKAVNEYKEAKELGVDTPVLVGPVTFLLSKPAKGVETFPPLSL 180  
QY 181 LGSILPIYKEVVAELKAAGASWIDLEPTLVKDLDAHELAAFSAYAELESSFSGLNVL 240  
DB 181 LDKILPYKEVIGELKAAGASWIDPDEPTLVLDLESHQLEAFTKAYSELESTLSGLNVIV 240  
QY 241 ETYFADIPAESYKTLTSLSGVTAVGFDLIRGAKTLDLIRSSFPSGKYLFAGVVDGRNIWA 300  
DB 241 ETYFADIPAEYTKILTALKGVTFGFDLVRGAKTLDLIKGFPSGKYLFAGVVDGRNIWA 300  
QY 301 DDLAASLSTLSLEAVAGKDLVSTSCSLMHTAVDLVNETKLDDEIKSWLAFAAQKVE 360  
DB 301 NDLAASLSTLSLEIGVSKDLVSTSCSLMHTAVDLVNEPKLDKEIKSWLAFAAQKVE 360  
QY 361 VNALAKALAGQKDEVYFAANAAQASRRSSPRVTNEEVQKAAALRGSDHRSTVTSARL 420  
DB 361 VNALAKALAGEKDEAFSEENAAQASRRSSPRVTNQAVQKAAALRGSDHRRATTVSARL 420  
QY 421 DAQQKLNLPVLPPTTIGSFQTVELRRVREYKAKKITEDEYISAIKEISKVKIQEE 480  
DB 421 DAQQKLNLPVLPPTTIGSFQTVLELRRVREYKAKKISEDDYVKAIKEISKVKIQEE 480

QY 481 LDIDVLVHGEPERNDMEYFGEQLSGFAFTANGWVQSYGSRGVKPPIIYGDVSRPNPMTV 540  
DB 481 LDIDVLVHGEPERNDMEYFGEQLSGFAFTANGWVQSYGSRGVKPPIIYGDVSRPNPMTV 540  
QY 541 FMSKMAQSMTPRPMKGMLTGPVTIILNWSFVRNDQPRFETCYQIALAIKKEVEDLEAAGIQ 600  
DB 541 FMSQTAQSMTRPMKGMLTGPVTIILNWSFVRNDQPRFETCYQIALAIKDEVEDLEKAGIN 600  
QY 601 VIQIDEAALREGLPRLKSEHAFYLDWAVHSFRITNCGVDTTQIHTMCSYFNNDITHSI 660  
DB 601 VIQIDEAALREGLPRLKAEHAFYLDWAVHSFRITNPLQDTTQIHTMCSYFNNDITHSI 660  
QY 661 IDMDADVITIENSRSDEKLISVFREGVKYGAGIGPGVYDIHSPRIPSTEBIADRVEXMLA 720  
DB 661 IDMDADVMTIENSRSSEKLISVFREGVKYGAGIGPGVYDIHSPRIPSTEBIADRINXMLA 720  
QY 721 VFDTNIIWMNPDCGLKTRKYTEVKPALTNMVSATKLIQTOLASAK 765  
DB 721 VLDTNIIWMNPDCGLKTRKYAEVKPALENMVSAAKLIRQTOLASAK 765

RESULT 5  
ABB93994  
ID ABB93994 standard; protein; 765 AA.  
AC ABB93994;  
XX  
DT 31-MAY-2002 (first entry)  
XX  
DE Herbicidally active polypeptide SEQ ID NO 3205.  
XX  
KW Herbicidal; plant; agriculture; herbicide.  
XX  
OS Arabidopsis thaliana.  
XX  
PN WO200210210-A2.  
XX  
PD 07-FEB-2002.  
XX  
PF 28-AUG-2001; 2001WO-EP009892.  
XX  
PR 28-AUG-2001; 2001WO-EP009892.  
XX  
PA (FARB ) BAYER AG.  
XX  
PI Tietjen K, Weidler M;  
XX  
DR WPI; 2002-269010/31.

PT Identifying plant target proteins for herbicidally active compounds,  
PT comprising aligning and comparing nucleic acid or amino acid sequences  
PT from plant with nucleic acid or amino acid sequences from non-plant  
PT organisms.  
XX  
PS Claim 5; SEQ ID NO 3205; 261pp + Sequence Listing; English.  
XX  
XX The invention relates to identifying target proteins (ABB90790-ABB94016)  
CC for herbicidally active compounds, comprising aligning and comparing  
CC nucleic acid or amino acid sequences from plant with nucleic acid or  
CC amino acid sequences from non-plant organisms using suitable search  
CC parameters, where plant sequences having an E-value greater by a factor  
CC of 3 than the E-value of most similar non-plant sequences are selected.  
CC The polypeptides or nucleic acids encoding them are useful for  
CC identifying modulators. The identified modulators are useful as  
CC herbicides  
XX  
SQ Sequence 765 AA;

Query Match 88.9%; Score 3472; DB 5; Length 765;  
Best Local Similarity 86.8%; Pred. No. 3.8e-282;  
Matches 664; Conservative 47; Mismatches 54; Indels 0; Gaps 0;

QY 1 MASHIVGYPRMGPKRELKFALESFWDGSSAEDLEKVAATDLRSSIWKOMSEAGIKYIPSN 60  
DB 1 MASHIVGYPRMGPKRELKFALESFWDGKSTABDLQKVSADLRSSIWKOMSAAGTKFIPSN 60  
QY 61 TSSYYDQVLDTTAMLGAVPERYSWTGGEIGLSTYFSMARGNATVPAMEMTKWFDTNHYFI 120  
DB 61 TFAHYDQVLDTTAMLGAVPPRYGYTGGEIGLDVYFSMARGNASVPAMEMTKWFDTNHYI 120  
QY 121 VPBLGSTKFTYASHKAVSEYKEAKALGIDTVPVLVGPVSYLLLSKPAKGVKSFSLSL 180  
DB 121 VPBLGPEVNFYSYASHKAVNEKEAKALGVDTPVLVGPVSYLLLSKAAGVDSFELLISL 180  
QY 181 LGSILPIYKEVVAELKAAGASWIQLDEPTLVKDLDAHELAFFSSAYAELESSFSGINVL 240  
DB 181 LPKILPIYKEVITELKAAGATWIOLEDPVLVMDLEGOKLQAFAGYAELESTLSGLNVLV 240  
QY 241 ETYFADIPAESYKTLTSLSGVTAYGFDLIRGAKTLDLIRSSFPSGKYLPAAGVVDGRNIWA 300  
DB 241 ETYFADIPAEAYKTLTSLKGVTAFGFDLVRGTKTLDLVKAGFPEGKYLPAAGVVDGRNIWA 300  
QY 301 DDLAASLSTLHSLAENVAGKDLVSTSCSLMHTAVDLVNETKLDDEIKSWLAFAAQKVE 360  
DB 301 NDFAASLSTLQALLEGIVGKDLVSTSCSLHTAVDLINETKLDDEIKSWLAFAAQKVE 360  
QY 361 VNALAKALAGQKDEEYFAANAAQAASRRSPRVNTEEVQKAAALRGSDHRRSTTVSARL 420  
DB 361 VNALAKALAGQKDEALFSANAAALASRRSSPRVTNEGVOKAAALKGSDDRATNVSARL 420  
QY 421 DAQOKLNLPLPTTIGSFPOTVELRRVREYKAKKITEDEYISAIKEISKVYKIOEB 480  
DB 421 DAQOKLNLPLPTTIGSFPOTVELRRVREYKAKKITEDEYISAIKEISKVYDLQEE 480  
QY 481 LDIDLVLHGEPERNDWEYFGEQLSGFAFTANGWQSYGSRCKPPIYGDVSRPNMTV 540  
DB 481 LDIDLVLHGEPERNDWEYFGEQLSGFAFTANGWQSYGSRCKPPIYGDVSRPKAMTV 540  
QY 541 FWSKMAQSMTPRPMKMLTGPVTILNWSFVRNDQPRFETCYQIALAIKKEVEDLEAAGIO 600  
DB 541 FWSAMAQSMTSRPMKMLTGPVTILNWSFVRNDQPRHETCYQIALAIKDEVEDLEKGGIG 600  
QY 601 VIQIDEALREGIPLRKSEHAFFYLDWAVHSFRITNCGVQDTQIHTMCSNFNDIHSI 660  
DB 601 VIQIDEALREGIPLRKSEHAFFYLDWAVHSFRITNCGVQDTQIHTMCSNFNDIHSI 660  
QY 661 IDMDADVITIENSRSDEKLLSVFREGVKYAGIGPGYDIHSPRIPSTEBIADRVKMLA 720  
DB 661 IDMDADVITIENSRSDEKLLSVFREGVKYAGIGPGYDIHSPRIPSSSEBIADRVNKMILA 720  
QY 721 VFDTNILWVNPDCGLKTRKYTEVKPALTNMVSATKLIQTOLASAK 765  
DB 721 VLEQNILWVNPDCGLKTRKYTEVKPALKNMVDAAKLIRSOLASAK 765  
RESULT 6  
ABB93525  
ID ABB93525 standard; protein; 765 AA.  
XX ABB93525;  
XX  
DT 31-MAY-2002 (first entry)  
XX  
DE Herbicidally active polypeptide SEQ ID NO 2736.  
XX  
KM Herbicidal; plant; agriculture; herbicide.  
OS Arabidopsis thaliana.  
XX  
PN WO200210210-A2.  
XX  
PD 07-FEB-2002.  
XX  
PF 28-AUG-2001; 2001WO-EP009892.  
XX

PR 28-AUG-2001; 2001WO-EP009892.  
XX  
XX (FARB ) BAYER AG.  
XX  
PI Tietjen K, Weidler M;  
XX  
XX WPI; 2002-269010/31.  
DR  
XX  
PT Identifying plant target proteins for herbicidally active compounds,  
PT comprising aligning and comparing nucleic acid or amino acid sequences  
PT from plant with nucleic acid or amino acid sequences from non-plant  
PT organisms.  
XX  
PS Claim 5; SEQ ID NO 2736; 261pp + Sequence Listing; English.  
XX  
XX The invention relates to identifying target proteins (ABB90790-ABB94016)  
CC for herbicidally active compounds, comprising aligning and comparing  
CC nucleic acid or amino acid sequences from plant with nucleic acid or  
CC amino acid sequences from non-plant organisms using suitable search  
CC parameters, where plant sequences having an E-value greater by a factor  
CC of 3 than the E-value of most similar non-plant sequences are selected.  
CC The polypeptides or nucleic acids encoding them are useful for  
CC identifying modulators. The identified modulators are useful as  
CC herbicides  
XX  
SQ Sequence 765 AA;  
Query Match 88.9%; Score 3472; DB 5; Length 765;  
Best Local Similarity 86.8%; Pred. No. 3.8e-282;  
Matches 664; Conservative 47; Mismatches 54; Indels 0; Gaps 0;  
QY 1 MASHIVGYPRMGPKRELKFALESFWDGSSAEDLEKVAATDLRSSIWKOMSEAGIKYIPSN 60  
DB 1 MASHIVGYPRMGPKRELKFALESFWDGKSTABDLQKVSADLRSSIWKOMSAAGTKFIPSN 60  
QY 61 TSSYYDQVLDTTAMLGAVPERYSWTGGEIGLSTYFSMARGNATVPAMEMTKWFDTNHYFI 120  
DB 61 TFAHYDQVLDTTAMLGAVPPRYGYTGGEIGLDVYFSMARGNASVPAMEMTKWFDTNHYI 120  
QY 121 VPBLGSTKFTYASHKAVSEYKEAKALGIDTVPVLVGPVSYLLLSKPAKGVKSFSLSL 180  
DB 121 VPBLGPEVNFYSYASHKAVNEKEAKALGVDTPVLVGPVSYLLLSKAAGVDSFELLISL 180  
QY 181 LGSILPIYKEVVAELKAAGASWIQLDEPTLVKDLDAHELAFFSSAYAELESSFSGINVL 240  
DB 181 LPKILPIYKEVITELKAAGATWIOLEDPVLVMDLEGOKLQAFAGYAELESTLSGLNVLV 240  
QY 241 ETYFADIPAESYKTLTSLSGVTAYGFDLIRGAKTLDLIRSSFPSGKYLPAAGVVDGRNIWA 300  
DB 241 ETYFADIPAEAYKTLTSLKGVTAFGFDLVRGTKTLDLVKAGFPEGKYLPAAGVVDGRNIWA 300  
QY 301 DDLAASLSTLHSLAENVAGKDLVSTSCSLMHTAVDLVNETKLDDEIKSWLAFAAQKVE 360  
DB 301 NDFAASLSTLQALLEGIVGKDLVSTSCSLHTAVDLINETKLDDEIKSWLAFAAQKVE 360  
QY 361 VNALAKALAGQKDEEYFAANAAQAASRRSPRVNTEEVQKAAALRGSDHRRSTTVSARL 420  
DB 361 VNALAKALAGQKDEALFSANAAALASRRSSPRVTNEGVOKAAALKGSDDRATNVSARL 420  
QY 421 DAQOKLNLPLPTTIGSFPOTVELRRVREYKAKKITEDEYISAIKEISKVYKIOEB 480  
DB 421 DAQOKLNLPLPTTIGSFPOTVELRRVREYKAKKITEDEYISAIKEISKVYDLQEE 480  
QY 481 LDIDLVLHGEPERNDWEYFGEQLSGFAFTANGWQSYGSRCKPPIYGDVSRPNMTV 540  
DB 481 LDIDLVLHGEPERNDWEYFGEQLSGFAFTANGWQSYGSRCKPPIYGDVSRPKAMTV 540  
QY 541 FWSKMAQSMTPRPMKMLTGPVTILNWSFVRNDQPRFETCYQIALAIKKEVEDLEAAGIO 600  
DB 541 FWSAMAQSMTSRPMKMLTGPVTILNWSFVRNDQPRHETCYQIALAIKDEVEDLEKGGIG 600  
QY 601 VIQIDEALREGIPLRKSEHAFFYLDWAVHSFRITNCGVQDTQIHTMCSNFNDIHSI 660  
DB 601 VIQIDEALREGIPLRKSEHAFFYLDWAVHSFRITNCGVQDTQIHTMCSNFNDIHSI 660

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Db      601 VIQIDEALREGLP L R K S E H A F Y L D W A V H S F R I T N C G V Q D S T Q I H T M C Y S H F N D I I H S I    660
Qy      661 IDMDADVITIENSRSDEKLISVFREGVKYGAGIGPGVYDIHSPRIIPSTEEIADRVEKMLA    720
        ||| | | | | | | | | | | | | | | | | | | | | | : | | | | | | | | | |
Db      661 IDMDADVITIENSRSDEKLISVFREGVKYGAGIGPGVYDIHSPRIIPSEEIADRVNKMILA    720
Qy      721 VFDTNILMVNPDCGLKTRKYTEVKPALTMVSATKLI RTQLASAK    765
        | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      721 VLEQNILMVNPDCGLKTRKYTEVKPALKNMVDAAKLIRSQLASAK    765

RESULT 7
ADE25084
ID      ADE25084 standard; protein; 765 AA.
XX
AC      ADE25084;
XX
DT      29-JAN-2004 (first entry)
XX
DE      Plant growth associated protein seq id 59.
XX
KW      plant growth; plant growth trait modulation; Brassicaceae; Arabidopsis;
KW      Brassica; Zea; Oryza; Triticum; Hordeum; Lolium; Sorghum; Glycine;
KW      Medicago; Helianthus; Lactuca; Beta; Vitis; Solanum; Lycopersicon;
KW      Capsicum; Gossypium; Hevea; Linum; Prunus; Citrus; Populus; Pinus;
KW      Quercus.
XX
OS      Magnoliophyta.
XX
PN      US2003188343-A1.
XX
PD      02-OCT-2003.
XX
PF      07-JAN-2003; 2003US-00338777.
XX
PR      09-JAN-2002; 2002US-0347288P.
PA      (LYNX-) LYNX THERAPEUTICS INC.
XX
PI      Bowen BA, Haudenschild CD, Buckler ES;
XX
DR      WPI; 2003-803305/75.
XX
N-PSDB; ADE25054.
PT      New isolated or recombinant polypeptide for use in modulating a plant
PT      growth trait in a flowering plant e.g. in Arabidopsis, Brassica, Zea, or
PT      Oryza.
XX
PS      Claim 8; SEQ ID NO 59; 81pp; English.
XX
CC      The invention describes an isolated or recombinant polypeptide (I)
CC      comprising a sequence: (a) comprising 1 of 30 sequences (S1), as given in
CC      the specification, or a conservative variant; (b) encoded by 1 of 30
CC      sequences (S2), as given in the specification, or a conservative variant;
CC      (c) encoded by a sequence that hybridises under stringent conditions to
CC      S2; and (d) encoded by a sequence 70 % identical to S2. The expression or
CC      activity of (I) is modulated to modulate a plant growth trait in a
CC      flowering plant, of the family Brassicaceae, preferably in a plant that
CC      is Arabidopsis, Brassica, Zea, Oryza, Triticum, Hordeum, Lolium, Sorghum,
CC      Glycine, Medicago, Helianthus, Lactuca, Beta, Vitis, Solanum,
CC      Lycopersicon, Capsicum, Gossypium, Hevea, Linum, Prunus, Citrus, Populus,
CC      Pinus, or Quercus. A new method is used to detect genes for a plant
CC      growth trait. This is the amino acid sequence of plant growth associated
CC      protein.
XX
SQ      Sequence 765 AA;

Query Match          88.8%; Score 3467; DB 7; Length 765;
Best Local Similarity 86.7%; Pred. No. 1e-281;
Matches 663; Conservative 47; Mismatches 55; Indels 0; Gaps 0;

1 MASHIVGYPRMGPKRELKFALSFWDGSSAEDLKVATDLRSSIMWQMSEAGIKYIPSN 60
||||| |:| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

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Db	1	MASHIVGYPRMGPKRELKFALESFWDGKSTAEDLQKVSADLRSSIMWKQMSAAGTKFIPSN	60
Qy	61	TSSYYDQVLDTTAMLGAVERYSWTGGEIGLSTYFSMARGNATVPAMEKTKMEDTNYHFI	120
Db	61	TFAYHDQVLDTTAMLGAVPPRYGTYGGEIGLDVYFSMARGNASVPAMEKTKMEDTNYHYI	120
Qy	121	VPBLGPSTKFTYASHKAVSEYKEAKALGIDTVPLVGPVSYLLLSKPAKVEKSFSLSL	180
Db	121	VPBLGPVNFYSYASHKAVNEYEAKALGVDTPVLVGPVSYLLLSKAAKGVDSFELLSL	180
Qy	181	IGSILPIYKEVVAELKAAGASWIODEPTLVKLDLDAHELAAFSASAYAELESSFSGLVLI	240
Db	181	LPKILPIYKEVITELKAAGATWIODEPVLVMDLEGOKLQAFGTGAYAELESTLSGLNVLV	240
Qy	241	ETYPADIPAESYKTLTSLSGVTAVGFDLIRGAKTLDLIRSSFPSGKYLPAGVVDGRNIWA	300
Db	241	ETYPADIPAEAYKTLTSLKGVTAFGFDLVRGTKTLDLVKAGFPEGKYLPAGVVDGRNIWA	300
Qy	301	DDLAAASLSTLHSLAVAGKDKLVSTSCSLMHTAVDLVNETKLDDEIKSWLFAAQKVE	360
Db	301	NDFAAASLSTLQALBEGIVGKDKLVSTSCSLHTAVDLINETKLDDEIKSWLFAAQKVE	360
Qy	361	VNALAKALAGQKDEVYFAANAAAQASRSSSPRVITNEEVQKAAALRGSHRSTTVSARL	420
Db	361	VNALAKALAGQKDEALFSANAAAASRRSSPRVTNEGQKAAALKGDHRRATNVSARL	420
Qy	421	DAQOKLNLPLPTTTIGSFPOTVELRVRREYKAKKITEDEYISAIBEISKVVKIOEE	480
Db	421	DAQOKLNLPLPTTTIGSFPOTVELRVRREYKAKKIVSEEDYVKAIKEIKKVVDLQEE	480
Qy	481	LDIDLVLHGEPERNDMVEYFGEOLSGFAFTANGWQSYGSRCSVKPPILYGDVSRPNMTV	540
Db	481	LDIDLVLHGEPERNDMVEYFGEOLSGFAFTANGWQSYGSRCSVKPPVIYGDVSRPKAMTV	540
Qy	541	FWSKMAQSMTPRPMKGMLTGPVTILNWSFVRNDQPRFETCYQIALAIKKEVEDLEAAGIQ	600
Db	541	FWSAMAQSMTSRPMKGMLTGPVTILNWSFVRNDQPRHETCYQIALAIKDEVEDLEKGGIG	600
Qy	601	VIQIDEAALREGLPLRKSEHAFLDMAVHSFRITNCGVODTQIHTHMCYSNPNDIHSI	660
Db	601	VIQIDEAALREGLPLRKSEHAFLDMAVHSFRITNCGVQDSTQIHTHMCYSHENDIHSI	660
Qy	661	IDMDADVITIENSRSDEKULSVFREGVKYGAGIGPGVYDIHSPRIPSTBEIADRVKMLA	720
Db	661	IDMDADVITIENSRSDEKULSVFREGVKYGAGIGPGVYDIHSPRIPSSBEIADRVNKMIA	720
Qy	721	VFDTNILMVNPDCGLKTRKYTEVVKPALTNMVSATKLIRTOLASAK 765	
Db	721	VLEONILMVNPDCGLKTRKYTEVVKPALKNMVDAAKLIRSOLASAK 765	

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RESULT 8
AAG53127
ID AAG53127 standard; protein; 765 AA.
XX
XX AAG53127;
AC
XX
XX 18-OCT-2000 (first entry)
DT
XX
XX Arabidopsis thaliana protein fragment SEQ ID NO: 67610.
DE
XX Protein identification; signal transduction pathway; metabolic pathway;
XX hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
XX
XX Arabidopsis thaliana.
OS
XX
XX EP1033405-A2.
PN
XX
XX 06-SEP-2000.
PD
XX
XX 25-FEB-2000; 2000EP-00301439.
PF
XX
XX

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PR 13-SEP-1999; 99US-0153758P.  
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Query Match 88.3%; Score 3448; DB 3; Length 765;  
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Matches 661; Conservative 46; Mismatches 58; Indels 0; Gaps 0;

QY 1 MASHIVGYPRMGPKRELKFALESFWDGSSAEDLEKVATDLRSSIWKQMSAIGIKYIPSN 60  
DB 1 MASHIVGYPRMGPKRELKFALESFWDGSSADDLQKVSADLRSDIWKQMSAAGIKYIPSN 60  
QY 61 TSSYYDOYLDTTAMLGAVPERYSWTGEGIGLSTYFSMARGNATVPAMEMTKMFDTNHYFI 120  
DB 61 TFSHYDOYLDTTAMLGAVPSRYGFTSGEIGLDVYFSMARGNASVPAMEMTKMFDTNHYI 120  
QY 121 VPGLGSTKFTYASHKAVSEYKEAKALGIDTVPVLVGPVSYLLSKPAKGVKSPSLSL 180  
DB 121 VPGLGPEYKFSYASHKAVNEYEKAKLGVETVPVLVGPVSYLLSKLAKGVKSPDLSTL 180  
QY 181 LGSILPIYKEVVAELKAAGASWIOLEPTLVKDLDAHELAAFSASVALESSFSGLNVL 240  
DB 181 LPKILPYKEVIAELKAAGASWIOLEBPLFVMDLEGHKLQAFSGAVALESTLSGLNVL 240  
QY 241 ETVFADIPAESYKTLTSLSGVTAYGFDLIRGAKTLDLIRSSFPSGKYLFAGVVDGRNIWA 300  
DB 241 ETVFADIPAEAYKTLTSLKGVTAFGFDLVRGTXTIDLKSGFPQGYLFAGVVDGRNIWA 300  
QY 301 DDLAASLSTLSLEAVAGKDLVSTSGSLMHTAVDLVNETKLDDEIKSWLAFAAQKVE 360  
DB 301 NDLAASLITLQSLGAVGKDLVSTSCSLHTAVDLINETKLDDEIKSWLAFAAQKVE 360  
QY 361 VNALAKALAGQKDEVYFAANAAAQASRRSSPRVTNEEVQAAAALRGSDHRRSTTVSARL 420  
DB 361 VDALAKALAGQTNESFFTANADALSSRRSSPRVTNESVQAAAALRGSDHRRSTTEVSARL 420  
QY 421 DAOQKLNLPVLPTTTIGSPQTVELRRVREYKAKKITEDEYISAIKEISIKVVKIQEE 480  
DB 421 DAOQKLNLPILPTTTIGSPQTVELRRVREYKAKKISEEDYKAIKEIKKVVIDIQED 480  
QY 481 LDIDVLVHGEPERNDMVEYFGEQLSGFAFTANGWQSYGSRVCVKPPIYGDVSRPNPMTV 540

DB 481 LDIDVLVHGEPERNDMVEYFGEQLSGFAFTANGWQSYGSRVCVKPPIYGDVSRPKPMTV 540  
QY 541 FWSKMAQSMTPRPMKMLTGPVTILNWSFVRNDQPRFETCYIALAIKKEVEDLEAGIQ 600  
DB 541 FWSSTAQSMTKRPMKMLTGPVTILNWSFVRNDQPRHETCYIALAIKDEVEDLEKGGIG 600  
QY 601 VIQIDEALREGLPLRKSEHAFYLDWAVHSFRITNCGVDPTQIHTMCSNFNDIHSI 660  
DB 601 VIQIDEALREGLPLRKAHSHFYLDWAVHSFRITNCGVDSTQIHTMCSNFNDIHSI 660  
QY 661 IDMDADVITIENSRSDEKLISVREGVKYGAGIGPGVYDIHSRIPSTBEIADRVKMLA 720  
DB 661 IDMDADVITIENSRSDEKLISVREGVKYGAGIGPGVYDIHSRIPSTBEIADRINKMLA 720  
QY 721 VFDTNIIWVNPDCGLKTRKYTEVKPALTMVSATKLIPTQLASAK 765  
DB 721 VLEQNIIMVNPDCGLKTRKYTEVKPALKAMVDAKLIHQLSGSAK 765

RESULT 9  
AAG18607  
ID AAG18607 standard; protein; 765 AA.  
XX AAG18607;  
AC AAG18607;  
XX 17-OCT-2000 (first entry)  
DT 17-OCT-2000 (first entry)  
XX Arabidopsis thaliana protein fragment SEQ ID NO: 20084.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 20084.  
XX Protein identification; signal transduction pathway; metabolic pathway;  
KW hybridisation assay; genetic mapping; gene expression control; promoter;  
KW termination sequence.  
XX Arabidopsis thaliana.  
OS Arabidopsis thaliana.  
PN EPI033405-A2.  
XX 06-SEP-2000.  
PD 06-SEP-2000.  
XX 25-FEB-2000; 2000EP-00301439.  
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DB 541 FWSSTAQSMTRKPMKGMTGPTVTLNWSFVRNDQPRHETCYQIALAIKDEVEDLEKGIG 600  
QY 601 VIQIDEALREGLPURKSEHAFLDWAHVSFRITNGVQDTQIHTHMCYSNFNDIHSI 660  
DB 601 VIQIDEALREGLPURKSEHAFLDWAHVSFRITNGVQDTQIHTHMCYSNFNDIHSI 660  
QY 661 IDMDADVITIENSRSDEKLSVFREGVKYAGIGPGVYDIHSPRIPSTEBIADRVEKMLA 720  
DB 661 IDMDADVITIENSRSDEKLSVFREGVKYAGIGPGVYDIHSPRIPSTEBIADRINKMLA 720  
QY 721 VFDTNLTWNPDCGLKTRKYTEVKPALTNMVSATKLIIRTQLASAK 765  
DB 721 VLEQNLTWNPDCGLKTRKYTEVKPALKAMVDAKLIIRSQLSAK 765

RESULT 11  
ADB23038  
ID ADB23038 standard; protein; 763 AA.

AC ADB23038;  
XX 20-NOV-2003 (first entry)  
DE Soybean methionine synthase.  
XX enzyme; plant; methionine synthase; methionine; seed; transformed plant;  
KW transgenic; soybean.  
XX Glycine max.

OS  
XX US2003088886-A1.  
PN 08-MAY-2003.

XX 28-JAN-2002; 2002US-00989339.  
XX 30-AUG-1995; 95US-0002973P.  
PR 27-AUG-1996; 96US-00703829.  
PR 19-AUG-1999; 99US-00377431.

XX (FALC/) FALCO S C.  
PA (FAMO/) FAMODU O O.  
PA (RAFA/) RAFALSKI J A.  
PA (RAMA/) RAMAKER M L.  
PA (TARC/) TARCZYNSKI M C.  
PA (THOR/) THORPE C.

XX Falco SC, Famodu OO, Rafalski JA, Ramaker ML, Tarczynski MC;  
PI Thorpe C;  
XX WPI; 2003-657990/62.  
DR N-PSDB; ADB23037.

XX New nucleic acid fragments encoding a plant 5-methyltetra-  
PT hydropteroyltriglutamate-homocysteine methyl transferase or methionine  
PT synthase, useful for producing increased levels of methionine in the  
PT seeds of transformed plants.

XX Example 1; Fig 2; 69pp; English.

XX The invention relates to an isolated nucleic acid fragment encoding a  
CC plant methionine synthase. The nucleic acid fragments and chimeric genes  
CC are useful for producing increased levels of methionine in the seeds of  
CC transformed plants. The present sequence represents the amino acid  
CC sequence of a plant methionine synthase.

XX Sequence 763 AA;

Query Match 86.9%; Score 3395; DB 6; Length 763;  
Best Local Similarity 85.4%; Pred. No. 1,1e-275;

Matches 651; Conservative 46; Mismatches 65; Indels 0; Gaps 0;

QY 1 MASHIVGPRMGKRELKFALESFWDGSSAEDLEKVATDLRSSIWKOMSEAGIKYIPSN 60  
DB 1 MASHIVGPRMGKRELKFALESFWDGSSAEDLQKVAADLRSSIWKOMAGAGIKYIPSN 60  
QY 61 TSSYYDQVLDLTAMLGAVPERYSWTGGEIGLSTYFSMARGNATVPAMENTKMFDTNYHFI 120  
DB 61 TFSFYDQLDATATLGAVPPRYGWTGGEIGFDTYFSMARGNATVPAMENTKMFDTNYHFI 120  
QY 121 VPBLGPSTKFTYASHKAVSEYKEAKALGIDTVPVLVGPVSYLLSKPAKGVKSFSLSL 180  
DB 121 VPBLGPDVNFTYASOKAVDEYKEAKALGVDTIIPVLVGPVYLLLSKPAKGVKSFSLSL 180  
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DB 181 LPKVLAVYKEVLAADKAAGASWIOFDEPTLVLDLESHKLOAFDTDAYAEIAPALSDLNLV 240  
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DB 241 ETYFADIPAEAYKTLTSLNGVTAYGFDLVGTHTLDLIKGFSPGKYLPAAGVDGRNIWA 300  
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DB 361 VNALAKALSGNKDVAFFSANAAQASRSSPRVTNEAVOKAAALRGSDHRRATNVSARL 420  
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DB 421 DAOQKLNLPILPTTIGSPQTVELRRVREYKANKISEEYVYSIKEIRKVELQEE 480  
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DB 601 VIQIDEALREGLPURKSEHAFLDWAHVSFRITNGVQDTQIHTHMCYSNFNDIHSI 660  
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DB 661 IDMDADVITIENSRSDEKLSVFREGVKYAGIGPGVYDIHSPRIPSTEBIADRINKMLA 720  
QY 721 VFDTNLTWNPDCGLKTRKYTEVKPALTNMVSATKLIIRTQLA 762  
DB 721 VLEKNLTWNPDCGLKTRKYTEVKPSONMVAAAKLIIRYELA 762

RESULT 12  
AAG18608  
ID AAG18608 standard; protein; 755 AA.

XX AAG18608;  
XX 17-OCT-2000 (first entry)

XX Arabidopsis thaliana protein fragment SEQ ID NO: 20085.

XX Protein identification; signal transduction pathway; metabolic pathway;  
KW hybridisation assay; genetic mapping; gene expression control; promoter;  
KW termination sequence.

OS Arabidopsis thaliana.

XX EP1033405-A2.

XX

PD 06-SEP-2000.  
XX  
PF 25-FEB-2000; 2000EP-00301439.  
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PR 25-FEB-1999; 99US-0121825P.  
PR 05-MAR-1999; 99US-0123180P.  
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Query Match 86.9%; Score 3394; DB 3; Length 755;

Best Local Similarity 86.2%; Pred. No. 1.3e-275;

Matches 651; Conservative 46; Mismatches 58; Indels 0; Gaps 0;

QY 11 MGPKRELKFALESFWDGKSSAEDLEKVAATDLRSSIWKMSEAGIKYIPSTSSYYDQVLD 70  
DB 1 MGPKRELKFALESFWDGKSSADDLQKVSADLRSDIWKMSSAAGIKYIPSTFSSHVDQVLD 60  
QY 71 TTAMLGAVPERYSWTGGEIGLSTYFSMARGNATVPAMENTKMPDTNHYHFLVPELGSTKF 130  
DB 61 TTAMLGAVPSRYGFTSGEIGLDVYFSMARGNASVPAMENTKMPDTNHYHFLVPELGPEVKF 120  
QY 131 TYASHKAVSEYKEAKALGIDTVPVLVGPVSYLLISKPAKGVKESFSLSLGSLPIYKE 190  
DB 121 SYASHKAVNEYKEAKALGVEIVPVLVGPVSYLLISKLAKGVDKSFDLSLLPKILPVYKE 180  
QY 191 VVAELKAAGASWLODEPTLVKDLDAHELAAFSAYAELESSFSGLNVLITYFADIPAE 250  
DB 181 VIAELKAAGASWLODEPLFVMDLEGHKLQAFSGAYAELESTLSGLNVLITYFADIPAE 240  
QY 251 SYKTLTSLGVTAYGFDLIRGAKTLDLIRSSPFGSKYLFAGVVDGRNIVADDLAASLSTL 310  
DB 241 AYKTLTSLKGVTAFGFDLVRGTKTIDLKSGFQGYLFAGVVDGRNIVANDLAASLITL 300  
QY 311 HSLAVAGKDKLVSTSCSLMHTAVDLVNETKLDDEIKSWLAFAPAKVVEVNALAKALAG 370  
DB 301 QSLBGVVGKDKLVSTSCSLMHTAVDLINETKDAEIKSWLAFAPAKVVEVDALAKALAG 360  
QY 371 QKDEVYFAANAQAASRSSPRVTNEEVOKAAALRGSDHRSTTVSARLDAQOKKLTLP 430  
DB 361 QTNESFFTANADALSSRRSSPRVTNESVOKAAALRGSDHRRRTTEVSARLDAQOKKLTLP 420  
QY\* 431 VLPTTTIGSPQIVELRVRREYKAKKITEDEYISAIKEISKVVKIQEELDIDLVLHGE 490  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

DB 421 ILPTTTIGSPQIVELRVRREYKAKKISEEDYVKAIKEIKKVVNDIQEEDIDLVLHGE 480  
QY 491 PERNDMVEYFGEOLSGFAFTANGWVQSYGRCYKBPITYGDVSRPNPMTVFWMSKWAQSM 550  
DB 481 PERNDMVEYFGEOLSGFAFTANGWVQSYGRCYKBPITYGDVSRPKPMTVFWMSSTAQSM 540  
QY 551 PRPMKMLTGPTVTLNWSFVRNDQPRFETCYQIALAIKKEVEDLEAAGIOVQIDEAALR 610  
DB 541 KRPKMGMLTGPTVTLNWSFVRNDQPRHETCYQIALAIKDEVEDLEKGGIGVQIDEAALR 600  
QY 611 EGLPLRKSSEHAFYLDVAVHSFRITNCGVQDTQIHTHMCYSNFNDIYHSIIDMDADVITI 670  
DB 601 EGLPLRKAHESFYLDVAVHSFRITNCGVQDSTQIHTHMCYSNFNDIYHSIIDMDADVITI 660  
QY 671 ENSRDEKLSVFRREGVKYAGIGPGVYDIHSPRIPSTEBIADRVKMLAVFDTNILMVN 730  
DB 661 ENSRDEKLSVFRREGVKYAGIGPGVYDIHSPRIPSTDEIADRINKMLAVLEQNILMVN 720  
QY 731 PDCGLKTRKYTEVVPALTNMVSATKLIRTOLASAK 765  
DB 721 PDCGLKTRKYTEVVPALKAMVDAKLIHQSGSAK 755

RESULT 13  
AAG53128  
ID AAG53128 standard; protein; 755 AA.  
XX AC AAG53128;  
XX DT 18-OCT-2000 (first entry)  
XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 67611.  
XX KW Protein identification; signal transduction pathway; metabolic pathway;  
KW hybridisation assay; genetic mapping; gene expression control; promoter;  
KW termination sequence.  
XX OS Arabidopsis thaliana.  
XX PN EPI033405-A2.  
XX PD 06-SEP-2000.  
XX PF 25-FEB-2000; 2000EP-00301439.  
XX PR 25-FEB-1999; 99US-0121825P.  
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PR 05-AUG-1999; 99US-0147260P.  
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PR 28-OCT-1999; 99US-0161992P.  
PR 28-OCT-1999; 99US-0161993P.  
PR 29-OCT-1999; 99US-0162142P.

Query Match 86.9%; Score 3394; DB 3; Length 755;  
Best Local Similarity 86.2%; Pred. No. 1.3e-275;  
Matches 651; Conservative 46; Mismatches 58; Indels 0; Gaps 0;

QY 11 MGPKEELKFALESFWDGKSSAEDLEKVAATDLRSSIWKQNSEAGIKYIPSNSSYYDQVLD 70  
DB 1 MGPKEELKFALESFWDGKSSADDLQKVSADLRSDIWKQNSAAGIKYIPSNFSHYDQVLD 60  
QY 71 TTAMLGAVPERYSWTGGEIGLSTYFSMARGNATVPAMENTKMFDTNHYHFIPELGPSTKF 130  
DB 61 TTAMLGAVPSRYGFTSGEIGLDVYFSMARGNASVPAMEMTKMFDNTNHYIPELGPVKF 120  
QY 131 TYASHKAVSEYKEAKALGIDTVPVLVGPVSYLLSKPAKGVKESFSLSLGSLPIYKE 190  
DB 121 SYASHKAVNEYKEAKALGVETVPVLVGPVSYLLSKLAKGVDKSFDLLSLPKILPYKE 180  
QY 191 VVAELKAAGASWIOLEPTLVKDLDAHELAAFSAYAELESSFSGNLVLIETYPADIPAE 250  
DB 181 VIAELKAAGASWIOLEBPLFWMLEGHKLQAFSGAYAELESTLSGLNLVETYPADIPAE 240  
QY 251 SYKTLTSLSGVTAYGFDLIRGAKTLDLIRSSFPSGKYLFAGVVDGRNIWADDLAASLSTL 310  
DB 241 AYKTLTSLKGVTAFGFDLVRGTXTIDLIKSGFPQKYLFAGVVDGRNIWADDLAASLITL 300  
QY 311 HSLAVAGKDKLVSTGSLMHTAVDLVNETKLDDEIKSWLAFAAQKVEVNALAKALAG 370  
DB 301 QSLGCVGKDKLVSTGSLMHTAVDLINETKLDDEIKSWLAFAAQKVEVNALAKALAG 360  
QY 371 QKDEVYFAANAAQAASRSSPRVTNEEVQKAAALRGSDHRRSTTVSARLDAQOKKLNLP 430  
DB 361 QTNESFTANADALSSRSSPRVTNESVQKAAALRGSDHRRRTTEVSARLDAQOKKLNLP 420  
QY 431 VLPTTIGSFPOTVELRRVRREYKAKKITEDEYISAIKEEISKVKIQEELDIDLVLHGE 490  
DB 421 ILPTTIGSFPOTVELRRVRREYKAKKISEEDYVKAIEEIKKVVDIQEELDIDLVLHGE 480  
QY 491 PERNDMEYFGEQSGFAFTANGWQSYGSRCPPIIYGDVSRPMTVFWMSMAQSMT 550  
DB 481 PERNDMEYFGEQSGFAFTANGWQSYGSRCPPIIYGDVSRPMTVFWMSMAQSMT 540  
QY 551 PRPMKGLTGPVTILNMSFVRNDQPRFETCYQIALAIKKEVEDLEAAGIQVIQIDEAALR 610  
DB 541 KRPMKGLTGPVTILNMSFVRNDQPRHETCYQIALAIKDEVEDLEKGGIGVQIDEAALR 600  
QY 611 EGLPLRKESEHAFYLDMAVHSFRITNGCVQDTQIHTHMCYSNFNDIHSIIDMADAVITI 670  
DB 601 EGLPLRKAHESFYLDMAVHSFRITNGCVQDSTQIHTHMCYSNFNDIHSIIDMADAVITI 660  
QY 671 ENSRDEKLSVREGVYKAGIGPGVYDIHSPRIPESTEEIADRVKMLAVEDTNILMVN 730  
DB 661 ENSRDEKLSVREGVYKAGIGPGVYDIHSPRIPESTDEIADRINKMLAVEQNILMVN 720  
QY 731 PDGGLTRKYTEVKPALTNMVSATKLIQTOLASAK 765  
DB 721 PDGGLTRKYTEVKPALKAMVDAKLIQSOLGSAK 755

RESULT 14  
ADA48634  
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XX  
AC ADA48634;  
XX  
DT 20-NOV-2003 (first entry)  
XX<sup>4</sup>  
DE Rice protein conferring disease resistance in plants.

XX  
KM disease resistance; pathogen tolerance; plant pathogen; plant; rice.  
XX  
OS Oryza sativa.  
XX  
PN WO2003000906-A2.  
XX  
XX  
PD 03-JAN-2003.  
XX  
PF 21-JUN-2002; 2002WO-1B002453.  
XX  
PR 22-JUN-2001; 2001US-0300112P.  
PR 26-SEP-2001; 2001US-0352277P.  
PR 22-MAR-2002; 2002US-0366535P.

(SYGN ) SYNGENTA PARTICIPATIONS AG.  
Glaizebrook J, Briggs S, Cooper B, Goff SA, Moughamer T;  
Katagiri F, Kreps J, Provart N, Ricke D, Zhu T;  
WPI; 2003-184052/18.  
N-PSDB; ADA48633.

PT New polynucleotide comprising a plant nucleotide sequence having an open  
PT reading frame that encodes a polypeptide associated with disease  
PT resistance, useful for conferring resistance or tolerance to a plant  
PT pathogen.  
XX  
PS Claim 10; SEQ ID NO 704; 299pp; English.  
XX

CC The invention relates to a novel isolated polynucleotide comprising a  
CC plant nucleotide sequence having an open reading frame that encodes a  
CC polypeptide associated with disease resistance or its fragment having  
CC substantially the same activity as the full-length polypeptide. The  
CC polynucleotide of the invention is useful for conferring resistance or  
CC tolerance to a plant pathogen. The present sequence represents a protein  
CC conferring disease resistance used in the invention.  
XX

Sequence 728 AA;

Query Match 86.0%; Score 3357.5; DB 6; Length 728;  
Best Local Similarity 84.5%; Pred. No. 1.5e-272;  
Matches 662; Conservative 29; Mismatches 19; Indels 73; Gaps 3;

QY 1 MASHIVGPRMGKRELKFALESFWDGKSSAEDLEKVAATDLRSSIWKQNSEAGIKYIPSN 60  
DB 1 MASHIVGPRMGKRELKFALESFWDGKSSAEDLEKVAATDLRASIMQWADAGIKYIPSN 60  
QY 61 TSSYYDQVLDTTAMLGAVPERYSWTGGEIGLSTYFSMARGNATVPAMENTKMFDTNHYFI 120  
DB 61 TFSYYDQVLDTTAMLGAVPERYSWTGGEIGLSTYFSMARGNATVPAMENTKMFDTNHYFI 120  
QY 121 VPBLGPSTKFTYASHKAVSEYKEAKALGIDTVPVLVGPVSYLLSKPAKGVKESFSLSL 180  
DB 121 VPBLGPNTKFSYSSHKAVNEYKEAKALGVDTVPVLVGPVSYLLSKPAKGVKESFALLSL 180  
QY 181 LGSILPIYKEVVAELKAAGASWIOLEPTLVKDLDAHELAAFSAYAELESSFSGNLVLI 240  
DB 181 LSSILPVYKEVVAELKAAGATWIOFDEPTLVLDLDSHQLAAFSAAYTEIESALSGLNLI 240  
QY 241 ETYPADIPAESYKTLTSLSGVTAYGFDLIRGAKTLDLIRSS-FPSGKYLFAGVVDGRNIW 299  
DB 241 ETYPADIPAESYKTLTSLNSVTAYGFDLIRGSKTLDLVKSAGFPSGKYLFAGVVDGRNIW 300

QY 300 ADDLAASLSTLHSLAVAGKDKLVSTGSLMHTAVDLVNETKLDDEIKSWLAFAAQKV 359  
DB 301 ADDLAASLSTLHSLAVAGKDKLVSTGSLMHTAVDLVNETKLDSEIKSWLAFAAQKV 360  
QY 360 EVNALAKALAGQKDE-----VYFAANAAQAASRSSPRVTNEBVQKAA 402  
DB 361 EVNALAKALAGQKDEHLKGLLIYTFVNNIVQAYFAANTAAQASRSSSPRVTNBEVQKAA 420  
QY 403 AALRGSDHRRSTTVSARLDAQOKKLNLPVLPTTTIGSFPOTVELRRVRREYKAKKITEDE 462

